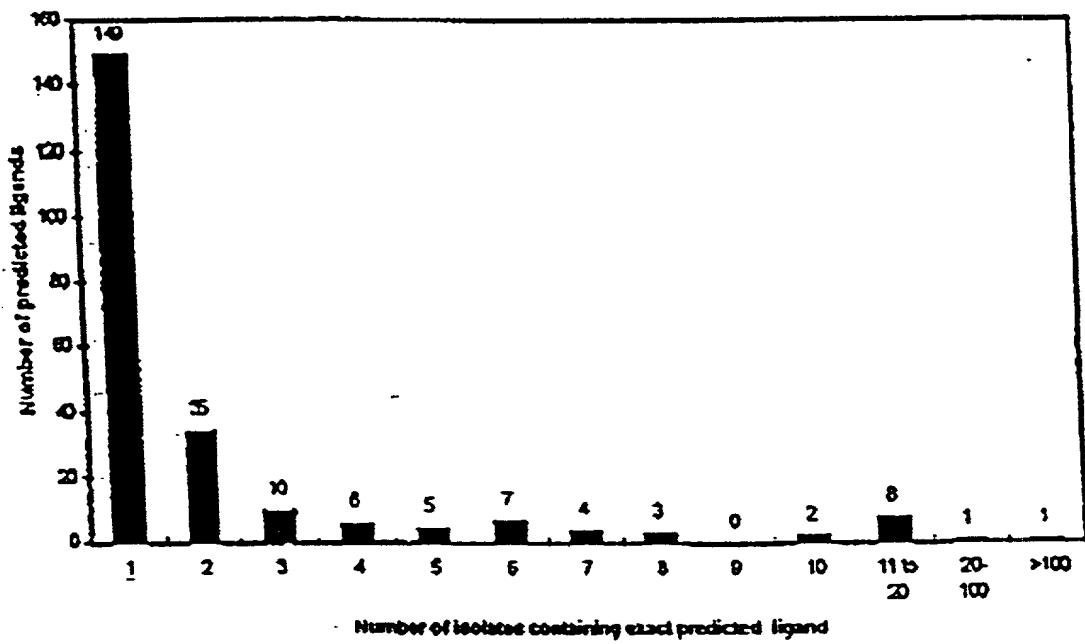


FIG. 1

a)



b)

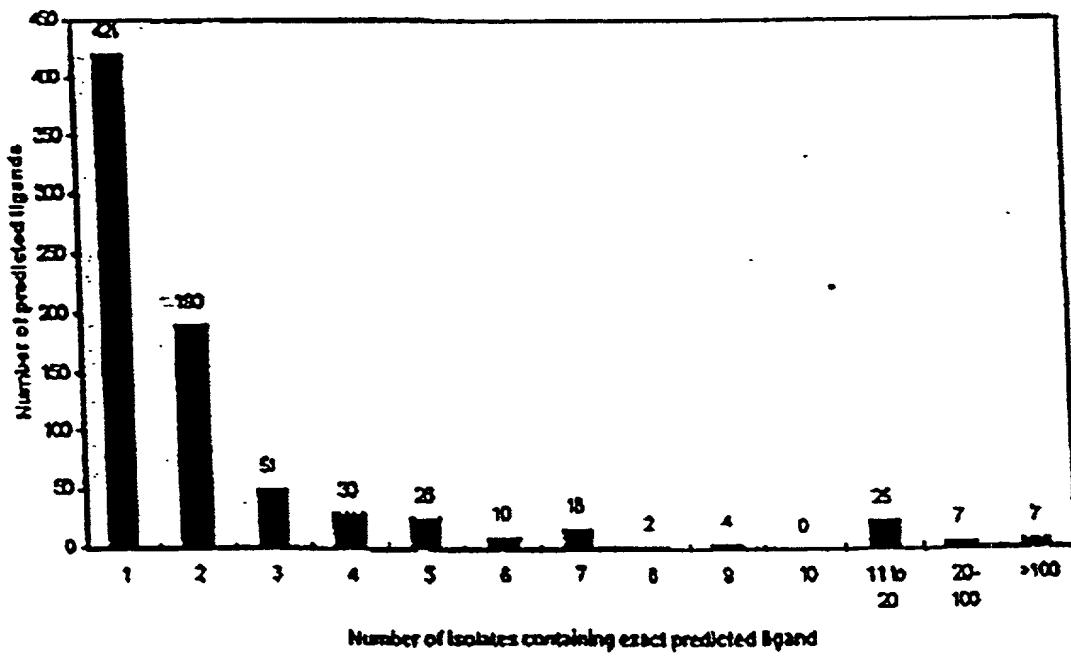


FIG. 3

Project Outline

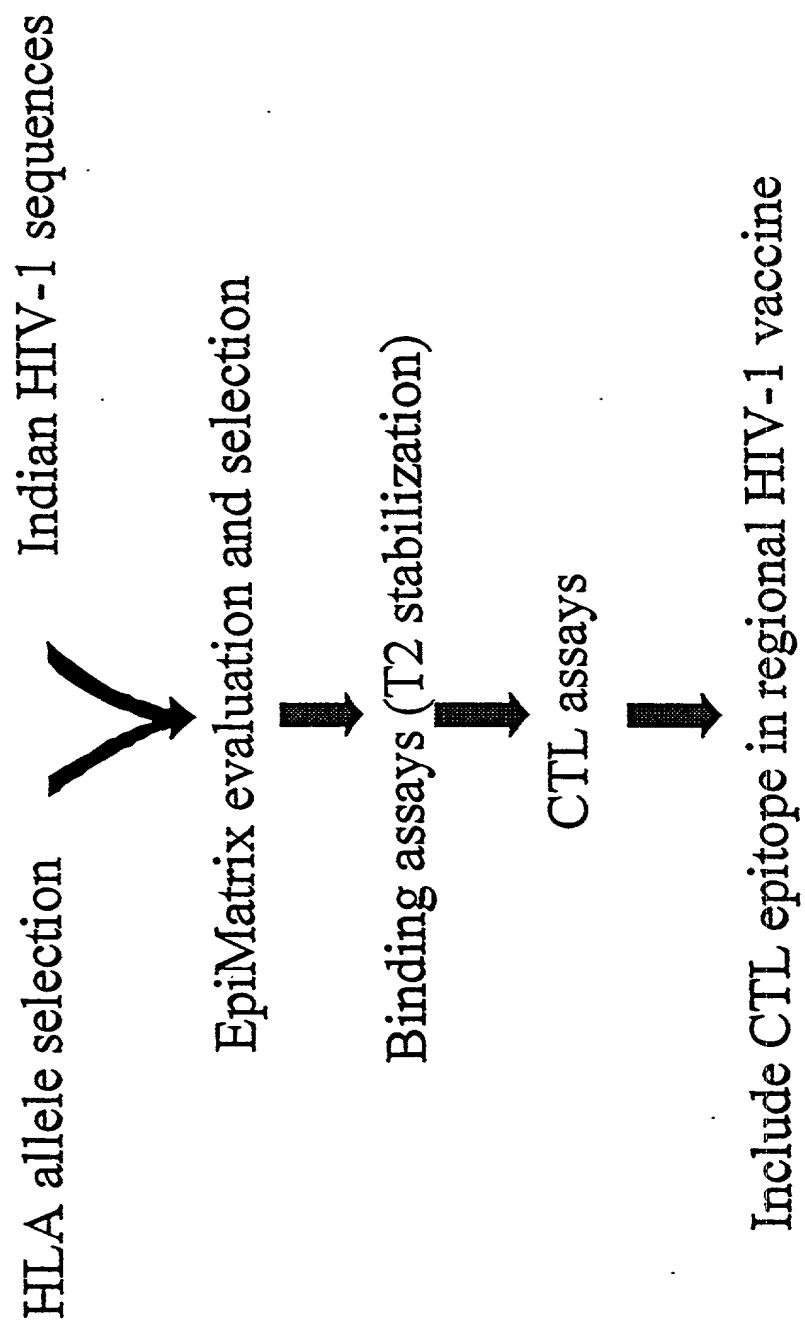
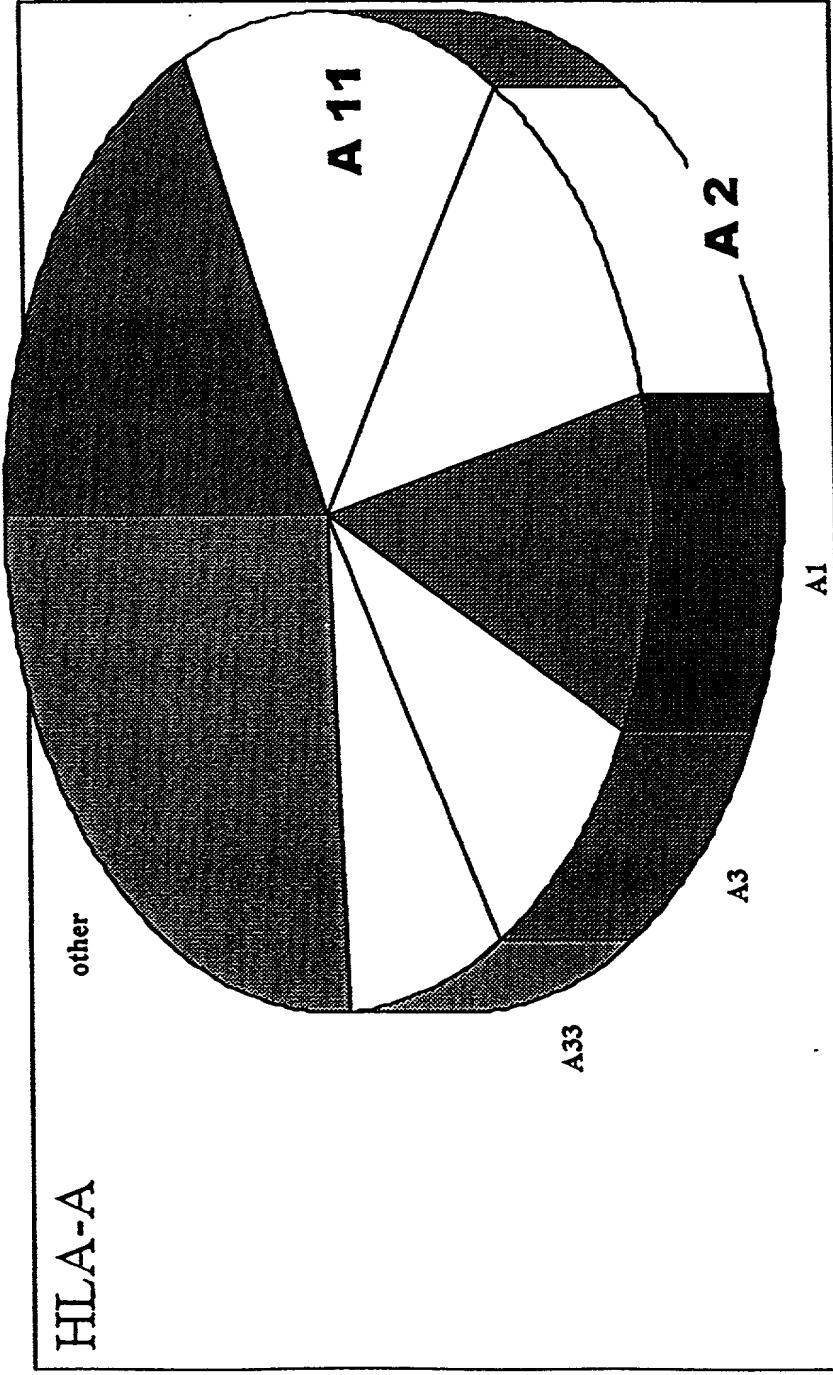


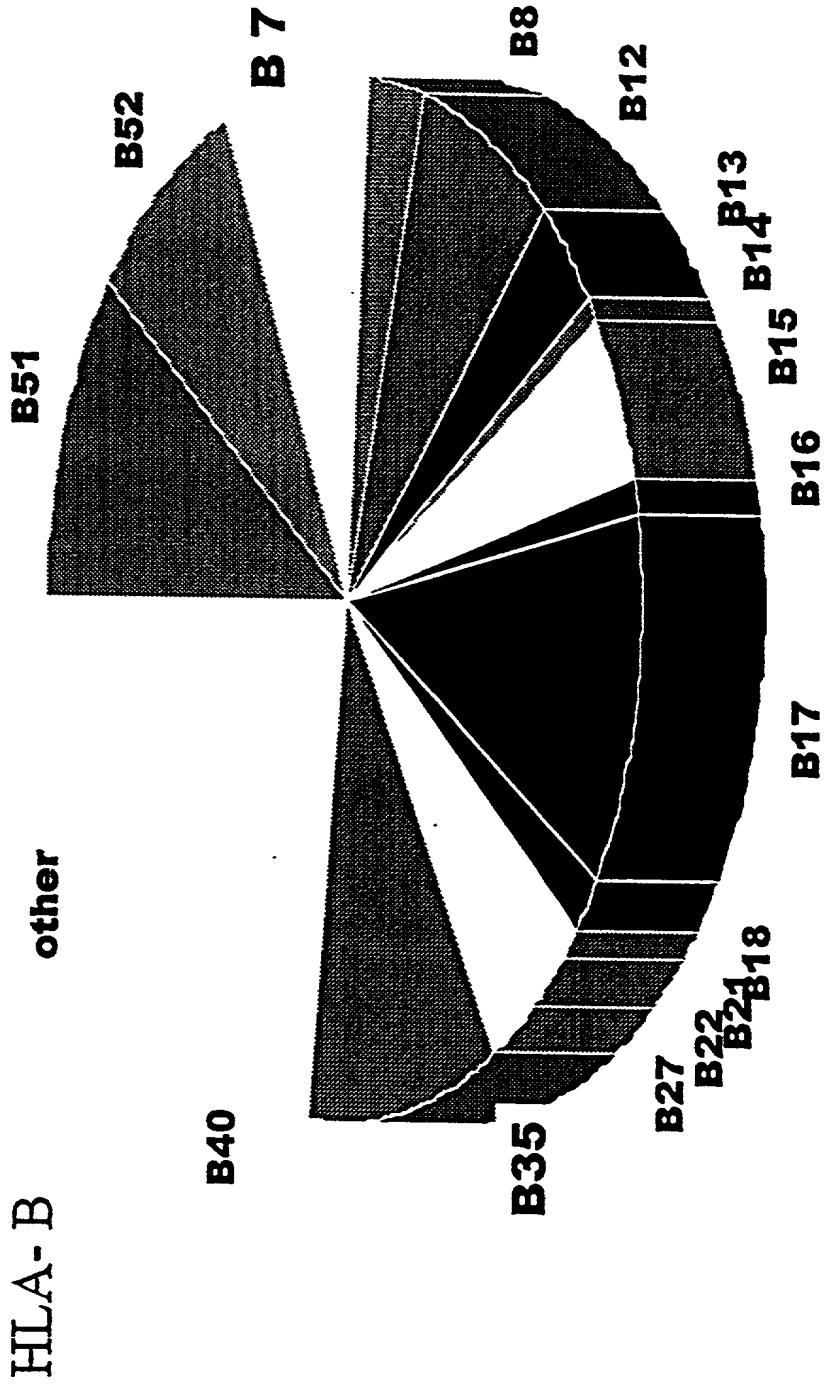
FIG. 4
Methods: HLA allele selection



HLA-A2 and -A11, -B7 and -B35 were selected for this pilot project due their prevalence of the HLA alleles in the Indian population....

FIG. 5

Methods: HLA allele selection



... and availability of cell lines for *in vitro* study.

FIG. 6
EpiMatrix Predictions and Binding Results: B 7
6 out of 7, and control peptide

B7										
Peptide #	Peptide	seq. Used	gene	strain	start-stop	% conserved	CTL	predicted EBP	avg MFI (200ug/ml)	avg fold Incr. (20ug/ml)
1	RPNINNTRKSI	RPNINNTRKSI	ENV	DID757	183-192	75	Y	8%	335.6	2.4
3	NPYNTPIFAL	NPYNTPIFAL	POL	Solnd5	61-70	60		20%	281.9	2.0
4	RAIEAQQQHLL	RAIEAQQQHLL	ENV	DID747	481-490	60		17%	181.5	1.3
5	TCKSNITGLL	TCKSNITGLL	ENV	DID780	375-384	59		18%	160.5	1.2
	KPVSTQLL	KPVSTQLL	ENV	DID747	182-191	71		46%	248.6	1.8
	KPCVKLTPLC	KPCVKLTPLC	ENV	DID747	51-60	100		27%	373.8	2.7
	GPKVKQWPL	GPKVKQWPL	POL	Solnd4	25-34	100		27%	314.7	2.3
	YPGIKVRLCL	YPGIKVRLCL	POL	Solnd4	278-287	100		28%	378.4	2.7

FIG. 7
EpiMatrix Predictions and Binding Results: B 35
7 out of 7 ... and control peptide

B37							
peptide #	peptide	seq. Used	gene	strain	start-stop	% conserved	predicted CTL
2	TVLDVGDAYF	TVLDVGDAYF	POL	Soln4	114-123	100	Y
6	EPPFLWMGY	EPPFLWMGY	POL	Soln4	231-239	100	9%
7	VPVKLKPQM	VPVKLKPQM	POL	Soln4	15-24	100	9%
8	CPKVTDFDPI	CPKVTDFDPI	ENV	DID760	144-153	53	7%
	KPVVSTQLL	KPVVSTQLL	ENV	DID747	182-191	71	9%
	KPCVVKLTPL	KPCVVKLTPL	ENV	DID747	51-80	100	11%
	GPKVKQWPLT	GPKVKQWPLT	POL	Soln4	25-34	100	11%
	YPGIKVRLC	YPGIKVRLC	POL	Soln4	278-287	100	7%

avg fold incr. (20ug/ml)

47.9

48.7

53.3

35.0

40.5

52.1

41.2

40.7

1.3

1.6

1.7

1.2

1.4

1.7

1.4

1.3

FIG. 8
EpiMatrix Predictions and Binding Results: A 2
3 out of 7 ... and control peptide

A2		peptide #	peptide	seq. Used	gene	strain	start-stop	% conserved	CTL	predicted EBF	avg MFI (200ug/ml)	avg fold incr. (20ug/ml)
13		ILKEPYHGV	ILKEPYHGVY	POL	Solnd4		316-325	80	Y	96%	1604.2	1.6
14		QLPEKDSWTV	QLPEKDSWTV	POL	Solnd4		252-261	100		87%	1388.1	1.4
15		NLWTYYGV	NLWTYYGV	ENV	GID1024		32-41	67		84%	1716.9	1.3
16		QMHEDVISL	QMHEDVISLW	ENV	DID747		37-46	91		78%	1413.1	1.4
17		KIEELREHLL	KIEELREHLL	POL	Solnd5		208-217	60		78%	889.9	0.9
18		DVNQNMHEDV	DMVNQNMHEDV	ENV	DID747		33-42	64		77%	731.1	0.4
19		GLKKKKSVTV	GLKKKKSVTV	POL	Solnd4		106-115	100		76%	1088.4	1.1
20		ELHPDKWTVQ	ELHPDKWTVQ	POL	Solnd4		240-249	80		72%	1048.1	1.0

FIG. 9
EpiMatrix Predictions and Binding Results: A 11
4 out of 7 ... and control peptide

A11										
Peptide #	peptide	seq. Used	gene	strain	start-stop	% conserved	CTL	predicted EBR	avg MFI (200ug/ml)	avg fold incr. (20ug/ml)
21	IYQEPFKNLK	IYQEPFKNLK	POL	Solnd4	348-357	100	Y	7%	677.5	3.1
22	VTFDPIPIHY	VTFDPIPIHY	ENV	DID760	147-156	53		22%	190.0	0.9
23	TVQCTHGIK	TVQCTHGIK	ENV	DID747	174-183	59		44%	733.4	3.3
24	NTPIFALKKK	NTPIFALKKK	POL	Solnd5	64-73	60		44%	187.8	0.9
25	LVDFRELNK	LVDFRELNK	POL	Solnd4	81-90	100		47%	755.2	3.4
26	PGMDGPKVKQ	PGMDGPKVKQ	POL	Solnd4	21-30	100		52%	193.8	0.7
27	GIPHPAGLKK	GIPHPAGLKK	POL	Solnd4	100-109	100		62%	309.6	1.4
28	FTTPDKKKHQK	FTTPDKKKHQK	POL	Solnd4	221-330	100		63%	920.6	4.1

FIG. 10
Methods: T2 Binding Assay

Allele matched peptides stabilize MHC molecules on the surface of TAP deficient cells. The stabilized MHC-peptide complex is detected using Ab to the MHC and fluorescence labeled secondary Ab.

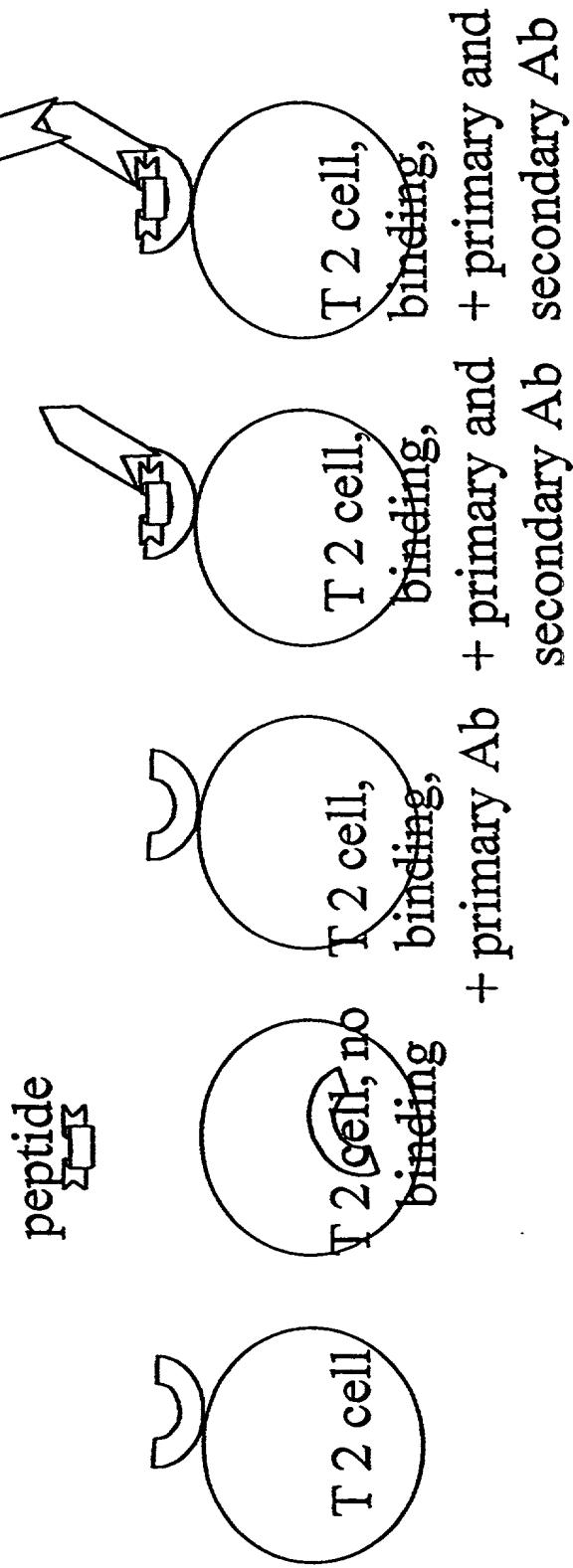


FIG. 11

Clustering of putative MHC ligands in *env*

